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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/973,424A

DATE: 05/09/2002

TIME: 12:54:04

Input Set : A:\cura85cip.txt

Output Set: N:\CRF3\05092002\I973424A.raw

3 <110> APPLICANT: Prayaga, Sudhirdas K
4 Taupier Jr, Raymond J
5 Bandaru, Raj
7 <120> TITLE OF INVENTION: NOVEL POLYPEPTIDES HOMOLOGOUS TO THYMOGIN, EPHRIN A
8 RECEPTORS, AND FIBROMODULIN, AND POLYNUCLEOTIDES
9 ENCODING SAME
11 <130> FILE REFERENCE: 15966-585 CIP2
13 <140> CURRENT APPLICATION NUMBER: 09/973,424A
14 <141> CURRENT FILING DATE: 2001-10-09
16 <150> PRIOR APPLICATION NUMBER: 60/159,805
17 <151> PRIOR FILING DATE: 1999-10-15
19 <150> PRIOR APPLICATION NUMBER: 60/159,992
20 <151> PRIOR FILING DATE: 1999-10-18
22 <150> PRIOR APPLICATION NUMBER: 60/160,952
23 <151> PRIOR FILING DATE: 1999-10-22
25 <150> PRIOR APPLICATION NUMBER: 09/689,486
26 <151> PRIOR FILING DATE: 2000-10-12
28 <150> PRIOR APPLICATION NUMBER: 09/687,276
29 <151> PRIOR FILING DATE: 2000-10-13
31 <160> NUMBER OF SEQ ID NOS: 84
33 <170> SOFTWARE: PatentIn Ver. 2.1
35 <210> SEQ ID NO: 1
36 <211> LENGTH: 430
37 <212> TYPE: DNA
38 <213> ORGANISM: Homo sapiens
40 <220> FEATURE:
41 <221> NAME/KEY: CDS
42 <222> LOCATION: (61)..(234)
44 <400> SEQUENCE: 1
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47 atg gca gac aaa cca gac ata ggg gaa atc gcc agc ttc aat aag gcc 108
48 Met Ala Asp Lys Pro Asp Ile Gly Glu Ile Ala Ser Phe Asn Lys Ala
49 1 5 10 15
51 aag ctg aag aaa aca gag atg cag gag aac acc ctg ctg acc aaa gag 156
52 Lys Leu Lys Lys Thr Glu Met Gln Glu Asn Thr Leu Leu Thr Lys Glu
53 20 25 30
55 gcc att gag cag gag aag cgg gtg aaa ttt cct aag agc ctg gag gat 204
56 Ala Ile Glu Gln Glu Lys Arg Val Lys Phe Pro Lys Ser Leu Glu Asp
57 35 40 45
59 tcc cta ccc ctg tca tct tcg aga ccc cag tagtaatgtg gaggaagaat 254
60 Ser Leu Pro Leu Ser Ser Arg Pro Gln
61 50 55
63 caccacaaga tggacacaag ccacaaactg tgacgtgaac ctggcactc cgtgctgatg 314

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65 ccaccagcct gagggtccct atgggtccaa tcagactgcc aaattctctg gtttgccctg 374
67 ggatattata gaaaattatt tgcgtgaata atgaaaacac agtcatggc aaaaaa 430
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71 <211> LENGTH: 58
72 <212> TYPE: PRT
73 <213> ORGANISM: Homo sapiens
75 <400> SEQUENCE: 2
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79 Lys Leu Lys Lys Thr Glu Met Gln Glu Asn Thr Leu Leu Thr Lys Glu
80     20          25          30
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83     35          40          45
85 Ser Leu Pro Leu Ser Ser Arg Pro Gln
86     50          55
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91 <211> LENGTH: 13
92 <212> TYPE: PRT
93 <213> ORGANISM: Homo sapiens
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108 cacggggact ggggctggct cacgtatccg gctcatgggt gggactccat caacgaggtg 180
109 gacgagtcct tccagccccat ccacacgtac caggttgc acgtcatgag ccccaaccag 240
110 aacaactggc tgcgcacgag ctgggtcccc cgagacggcg cccggcgcgt ctatgctgag 300
111 atcaagttt ccctgcgcga ctgcaacacgc atgcctggtg tgctggc ac ctgcaaggag 360
112 accttcaacc tctactacct ggagtccggac cgcacactgg gggccagcac acaagaaagc 420
113 cagttccctca aaatcgacac cattgcggcc gacgagagct tcacaggtgc cgaccttgg 480
114 gtgcggcgctc tcaagctcaa cacggaggtg cgcaactgtgg gtcccctcaag caagcgcggc 540
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121 gctccagccg cccaaacccctg ccactgtgac ttcagactact accgtgcagc cctggaccccg 960
122 ccgtccctcg cctgcaccccg gccaccctcg gcaccaggta acctgatctc cagtgtgaat 1020
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124 acctacaatcg ccgtgtccgc ccgctgcccc tggcactga gccgctgcga ggcatgtggg 1140
125 agcggcaccgc gcttggcc ccagcagaca agcctggtc aggccagcct gctggggcc 1200
126 aacctgctgg cccacatgaa ctactccctc tggatcgagg ccgtcaatgg cgtgtccgac 1260
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 129 caggagcccc agcagccgaa cggcatcata ctggagtatg agatcaagta ctacgagaag 1440
 130 gacaaggaga tgcagagcta ctccaccctc aaggccgtca ccaccagagc caccgtctcc 1500
 131 ggcctcaagc cggcacccg ctacgttgc caggccgag cccgcaccc agcaggctgt 1560
 132 ggccgcttca gccaggccat ggagggtggag accggaaac cccggccccc ctatgacacc 1620
 133 aggaccattg tctggatctg cctgacgctc atcacggcc tggtggtgt tctgctctg 1680
 134 ctcatctgca agaagaggca ctgtggctac agcaaggcc tccaggactc ggacgaggag 1740
 135 aagatgcact atcagaatgg acaggcaccc ccacctgtct tcctgcctct gcatcacc 1800
 136 cgggaaagc tcccagagcc ccagtttat gggaaacccc acacctacga ggagccaggc 1860
 137 cggcgggcc gcagttcac tcgggagatc gaggcctta gatatccat cgagaaaatc 1920
 138 atcggctctg gagactccgg ggaagtctgc tacgggaggc tgcgggtgcc agggcagcgg 1980
 139 gatgtccccg tggccatcaa ggcctcaaa gccgttaca cggagagaca gaggcgggac 2040
 140 ttccctgagcg aggctccat catggggaa ttccgaccat ccaacatcat ccgcctcgag 2100
 141 ggtgtcgta cccgtggccg cctggcaatg attgtactg agtacatgga gaacggctct 2160
 142 ctggacacct tcctgaggac ccacgacggg cagtttacca tcatgcagct ggtggcatg 2220
 143 ctgagaggag tgggtccgg catgcgtac ctctcagacc tggctatgt ccaccgagac 2280
 144 ctggccccc gcaacgttctt ggttacacgc aacctggctc gcaagggtgt tgacttcggg 2340
 145 ctctcacggg tgctggagga cgacccggat gctgcctaca ccaccacggg cgggaagatc 2400
 146 cccatccgtt ggacggccccc agaggccatc gccttccgca cttctctctc ggccagcgc 2460
 147 gtgtggagct tcggcgttgtt catgtggag gtgtggct atggggagcg gcccactgg 2520
 148 aacatgacca accgggatgt gatcagctt gtggaggagg ggtaccgc gcccgcaccc 2580
 149 atgggctgcc cccacgcctt gcaccagctc atgctcact gttggcaca ggaccggcgg 2640
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 151 agtctcacgg ccaccgcac agtcagcagg tgccaccccc ctgcctcgt ccggagctgc 2760
 152 ttgacccctc gaggggcag cgggtggcggt gggggctca ccgtggggga ctggctggac 2820
 153 tccatccgca tggccggta ccgagaccac ttcgtctggc gcggataactc ctctctggc 2880
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 160 <211> LENGTH: 992
 161 <212> TYPE: PRT
 162 <213> ORGANISM: Homo sapiens
 164 <400> SEQUENCE: 5
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 168 Ala Ala Ala Ala Ala Ala Thr Cys Val Ser Ala Ala Arg Gly Glu Val
 169 20 25 30
 171 Asn Leu Leu Asp Thr Ser Thr Ile His Gly Asp Trp Gly Trp Leu Thr
 172 35 40 45
 174 Tyr Pro Ala His Gly Trp Asp Ser Ile Asn Glu Val Asp Glu Ser Phe
 175 50 55 60
 177 Gln Pro Ile His Thr Tyr Gln Val Cys Asn Val Met Ser Pro Asn Gln
 178 65 70 75 80
 180 Asn Asn Trp Leu Arg Thr Ser Trp Val Pro Arg Asp Gly Ala Arg Arg
 181 85 90 95
 183 Val Tyr Ala Glu Ile Lys Phe Thr Leu Arg Asp Cys Asn Ser Met Pro
 184 100 105 110
 186 Gly Val Leu Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Leu Glu

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189 Ser	Asp Arg Asp Leu Gly Ala Ser	Thr Gln Glu Ser	Gln Phe Leu Lys	
190	130	135	140	
192 Ile Asp Thr Ile Ala Ala Asp	Glu Ser Phe Thr	Gly Ala Asp Leu Gly		
193	145	150	155	160
195 Val Arg Arg Leu Lys Leu Asn	Thr Glu Val Arg Ser	Val Gly Pro Leu		
196	165	170	175	
198 Ser Lys Arg Gly Phe Tyr Leu Ala	Phe Gln Asp Ile	Gly Ala Cys Leu		
199	180	185	190	
201 Ala Ile Leu Ser Leu Arg Ile	Tyr Tyr Lys Lys Cys	Pro Ala Met Val		
202	195	200	205	
204 Arg Asn Leu Ala Ala Phe Ser	Glu Ala Val Thr	Gly Ala Asp Ser Ser		
205	210	215	220	
207 Ser Leu Val Glu Val Arg Gly	Gln Cys Val Arg His	Ser Glu Glu Arg		
208	225	230	235	240
210 Asp Thr Pro Lys Met Tyr Cys	Ser Ala Glu Gly	Glu Trp Leu Val Pro		
211	245	250	255	
213 Ile Gly Lys Cys Val Cys Ser	Ala Gly Tyr Glu Glu Arg Arg Asp Ala			
214	260	265	270	
216 Cys Val Ala Cys Glu Leu Gly	Phe Tyr Lys Ser Ala Pro	Gly Asp Gln		
217	275	280	285	
219 Leu Cys Ala Arg Cys Pro Pro	His Ser His Ser Ala Ala Pro	Ala Ala		
220	290	295	300	
222 Gln Ala Cys His Cys Asp Leu	Ser Tyr Tyr Arg Ala Ala Leu Asp Pro			
223	305	310	315	320
225 Pro Ser Ser Ala Cys Thr Arg	Pro Pro Ser Ala Pro	Val Asn Leu Ile		
226	325	330	335	
228 Ser Ser Val Asn Gly Thr Ser	Val Thr Leu Glu Trp Ala Pro	Pro Leu		
229	340	345	350	
231 Asp Pro Gly Gly Arg Ser Asp	Ile Thr Tyr Asn Ala Val	Cys Arg Arg		
232	355	360	365	
234 Cys Pro Trp Ala Leu Ser Arg	Cys Glu Ala Cys Gly	Ser Gly Thr Arg		
235	370	375	380	
237 Phe Val Pro Gln Gln Thr Ser	Leu Val Gln Ala Ser	Leu Leu Val Ala		
238	385	390	395	400
240 Asn Leu Leu Ala His Met Asn	Tyr Ser Phe Trp Ile	Glu Ala Val Asn		
241	405	410	415	
243 Gly Val Ser Asp Leu Ser Pro	Glu Pro Arg Arg Ala Ala Val	Val Val Asn		
244	420	425	430	
246 Ile Thr Thr Asn Gln Ala Ala	Pro Ser Gln Val Val	Val Ile Arg Gln		
247	435	440	445	
249 Glu Arg Ala Gly Gln Thr Ser	Val Ser Leu Leu Trp Gln Glu Pro	Glu		
250	450	455	460	
252 Gln Pro Asn Gly Ile Ile	Leu Glu Tyr Glu Ile	Lys Tyr Tyr Glu Lys		
253	465	470	475	480
255 Asp Lys Glu Met Gln Ser Tyr	Ser Thr Leu Lys Ala Val Thr	Thr Arg		
256	485	490	495	
258 Ala Thr Val Ser Gly Leu Lys	Pro Gly Thr Arg Tyr Val	Phe Gln Val		
259	500	505	510	

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261 Arg Ala Arg Thr Ser Ala Gly Cys Gly Arg Phe Ser Gln Ala Met Glu
 262 515 520 525
 264 Val Glu Thr Gly Lys Pro Arg Pro Arg Tyr Asp Thr Arg Thr Ile Val
 265 530 535 540
 267 Trp Ile Cys Leu Thr Leu Ile Thr Gly Leu Val Val Leu Leu Leu
 268 545 550 555 560
 270 Leu Ile Cys Lys Lys Arg His Cys Gly Tyr Ser Lys Ala Phe Gln Asp
 271 565 570 575
 273 Ser Asp Glu Glu Lys Met His Tyr Gln Asn Gly Gln Ala Pro Pro Pro
 274 580 585 590
 276 Val Phe Leu Pro Leu His His Pro Pro Gly Lys Leu Pro Glu Pro Gln
 277 595 600 605
 279 Phe Tyr Ala Glu Pro His Thr Tyr Glu Glu Pro Gly Arg Ala Gly Arg
 280 610 615 620
 282 Ser Phe Thr Arg Glu Ile Glu Ala Ser Arg Ile His Ile Glu Lys Ile
 283 625 630 635 640
 285 Ile Gly Ser Gly Asp Ser Gly Glu Val Cys Tyr Gly Arg Leu Arg Val
 286 645 650 655
 288 Pro Gly Gln Arg Asp Val Pro Val Ala Ile Lys Ala Leu Lys Ala Gly
 289 660 665 670
 291 Tyr Thr Glu Arg Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser Ile Met
 292 675 680 685
 294 Gly Gln Phe Asp His Pro Asn Ile Ile Arg Leu Glu Gly Val Val Thr
 295 690 695 700
 297 Arg Gly Arg Leu Ala Met Ile Val Thr Glu Tyr Met Glu Asn Gly Ser
 298 705 710 715 720
 300 Leu Asp Thr Phe Leu Arg Thr His Asp Gly Gln Phe Thr Ile Met Gln
 301 725 730 735
 303 Leu Val Gly Met Leu Arg Gly Val Gly Ala Gly Met Arg Tyr Leu Ser
 304 740 745 750
 306 Asp Leu Gly Tyr Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val
 307 755 760 765
 309 Asp Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Val
 310 770 775 780
 312 Leu Glu Asp Asp Pro Asp Ala Ala Tyr Thr Thr Thr Gly Gly Lys Ile
 313 785 790 795 800
 315 Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ala Phe Arg Thr Phe Ser
 316 805 810 815
 318 Ser Ala Ser Asp Val Trp Ser Phe Gly Val Val Met Trp Glu Val Leu
 319 820 825 830
 321 Ala Tyr Gly Glu Arg Pro Tyr Trp Asn Met Thr Asn Arg Asp Val Ile
 322 835 840 845
 324 Ser Ser Val Glu Glu Gly Tyr Arg Leu Pro Ala Pro Met Gly Cys Pro
 325 850 855 860
 327 His Ala Leu His Gln Leu Met Leu Asp Cys Trp His Lys Asp Arg Ala
 328 865 870 875 880
 330 Gln Arg Pro Arg Phe Ser Gln Ile Val Ser Val Leu Asp Ala Leu Ile
 331 885 890 895
 333 Arg Ser Pro Glu Ser Leu Arg Ala Thr Ala Thr Val Ser Arg Cys Pro

VERIFICATION SUMMARY

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